```
┌─────────────────────────────────────────────────────────────┐
│  This Raw Listing contains the General Information           │
│  Section and up to first 5 pages.                           │
└─────────────────────────────────────────────────────────────┘
```

ENTERED

```
 1    <110> APPLICANT: Georgopoulos, Katia
 2          Morgan, Bruce
 3    <120> TITLE OF INVENTION: AIOLOS GENE
 4    <130> FILE REFERENCE: 10287/031001
 5    <140> CURRENT APPLICATION NUMBER: US/09/019,348
 6    <141> CURRENT FILING DATE: 1998-02-05.
 7    <150> EARLIER APPLICATION NUMBER: US 08/733,622
 8    <151> EARLIER FILING DATE: 1996-10-17
 9    <150> EARLIER APPLICATION NUMBER: US 60/017,646
10    <151> EARLIER FILING DATE: 1996-05-14
11    <150> EARLIER APPLICATION NUMBER: US 60/005,527
12    <151> EARLIER FILING DATE: 1995-10-18
13    <160> NUMBER OF SEQ ID NOS: 29
14    <170> SOFTWARE: FastSEQ for Windows Version 3.0
15    <210> SEQ ID NO 1
16    <211> LENGTH: 1984
17    <212> TYPE: DNA
18    <213> ORGANISM: Mus musculus
19    <220> FEATURE:
20    <221> NAME/KEY: CDS
21    <222> LOCATION: (374)...(1894)
22    <400> SEQUENCE: 1
23        cacgagcgca caccgctcgg ctctccttgc gacacgccct catccccggt gtttctcaag        60
24        tagacgtccc gagacggtcg ctgaggcact gtttccacgc gatcagggtt cctcaggctt       120
25        gacattcaaa agtgggtgcg gaacccgcgg cactcggagc gtgctttaaa gcggccgcca       180
26        gccagcgccg ctctaacctc gcgccccggc tgccggcggc tcccgccctg catctgcgcc       240
27        gacgcgaccg agcgatcccg gggcctccct gcgcccggaa tctcccgcca gccgcgcggg       300
28        tccccacggc agcagcacgt ggagcggccg cggagcctga gcgacagctg cagcccgcgc       360
29        ggcccgcggc gac atg gaa gat ata caa ccg act gtg gag ctg aaa agc        409
30                    Met Glu Asp Ile Gln Pro Thr Val Glu Leu Lys Ser
31                     1               5                      10
32        acg gag gag cag cct ctg ccc aca gag agc cca gac gct ctg aat gac       457
33        Thr Glu Glu Gln Pro Leu Pro Thr Glu Ser Pro Asp Ala Leu Asn Asp
34                 15                  20                      25
35        tac agc ttg ccc aaa cct cat gag ata gaa aac gtg gac agt aga gaa       505
36        Tyr Ser Leu Pro Lys Pro His Glu Ile Glu Asn Val Asp Ser Arg Glu
37             30                  35                      40
38        gcc cca gcc aat gaa gac gaa gat gca gga gaa gat tcg atg aaa gtg       553
39        Ala Pro Ala Asn Glu Asp Glu Asp Ala Gly Glu Asp Ser Met Lys Val
40         45                  50                      55                60
41        aaa gat gaa tac agc gac aga gat gag aac att atg aag ccg gag ccc       601
42        Lys Asp Glu Tyr Ser Asp Arg Asp Glu Asn Ile Met Lys Pro Glu Pro
43                 65                  70                      75
44        atg gga gat gca gaa gag agt gaa atg cct tac agc tat gca aga gaa       649
```

```
45        Met Gly Asp Ala Glu Glu Ser Glu Met Pro Tyr Ser Tyr Ala Arg Glu
46                        80                    85                    90
47        tac agc gac tat gaa agc att aag ctg gag aga cac gtg ccc tat gac    697
48        Tyr Ser Asp Tyr Glu Ser Ile Lys Leu Glu Arg His Val Pro Tyr Asp
49                        95                   100                   105
50        aac agc aga cca acc agt ggg aag atg aac tgc gac gtg tgc ggg tta    745
51        Asn Ser Arg Pro Thr Ser Gly Lys Met Asn Cys Asp Val Cys Gly Leu
52                       110                   115                   120
53        tcc tgc att agc ttc aac gtc ttg atg gtt cat aag cga agc cat acc    793
54        Ser Cys Ile Ser Phe Asn Val Leu Met Val His Lys Arg Ser His Thr
55        125                   130                   135                   140
56        ggc gaa cgc ccg ttc cag tgt aat cag tgc ggg gca tct ttt act cag    841
57        Gly Glu Arg Pro Phe Gln Cys Asn Gln Cys Gly Ala Ser Phe Thr Gln
58                       145                   150                   155
59        aaa ggt aac ctc ctc cgt cat att aaa ctg cac acg ggg gaa aaa cct    889
60        Lys Gly Asn Leu Leu Arg His Ile Lys Leu His Thr Gly Glu Lys Pro
61                       160                   165                   170
62        ttt aag tgt cac ctc tgc aac tac gca tgc caa agg aga gat gcg ctc    937
63        Phe Lys Cys His Leu Cys Asn Tyr Ala Cys Gln Arg Arg Asp Ala Leu
64                       175                   180                   185
65        acg gga cac ctt agg aca cat tct gtg gag aag ccg tac aag tgt gag    985
66        Thr Gly His Leu Arg Thr His Ser Val Glu Lys Pro Tyr Lys Cys Glu
67                       190                   195                   200
68        ttc tgc gga aga agc tac aag cag aga agc tcc ctg gag gag cac aag   1033
69        Phe Cys Gly Arg Ser Tyr Lys Gln Arg Ser Ser Leu Glu Glu His Lys
70        205                   210                   215                   220
71        gaa cgc tgc cga gct ttt ctt cag aac cct gac ctg ggg gac gct gca   1081
72        Glu Arg Cys Arg Ala Phe Leu Gln Asn Pro Asp Leu Gly Asp Ala Ala
73                       225                   230                   235
74        agt gtg gag gca aga cac atc aaa gcc gag atg gga agt gag aga gct   1129
75        Ser Val Glu Ala Arg His Ile Lys Ala Glu Met Gly Ser Glu Arg Ala
76                       240                   245                   250
77        ctc gtc ctg gac aga tta gca agc aat gtg gct aag cga aaa agc tcg   1177
78        Leu Val Leu Asp Arg Leu Ala Ser Asn Val Ala Lys Arg Lys Ser Ser
79                       255                   260                   265
80        atg cct cag aaa ttc atc ggt gag aag cgg cac tgc ttc gat gcc aac   1225
81        Met Pro Gln Lys Phe Ile Gly Glu Lys Arg His Cys Phe Asp Ala Asn
82        270                   275                   280
83        tac aat ccc ggc tac atg tac gag aag gag aac gag atg atg cag acc   1273
84        Tyr Asn Pro Gly Tyr Met Tyr Glu Lys Glu Asn Glu Met Met Gln Thr
85        285                   290                   295                   300
86        cgg atg atg gac caa gcc atc aat aac gcc atc ag: tat cta ggg gct   1321
87        Arg Met Met Asp Gln Ala Ile Asn Asn Ala Ile Ser Tyr Leu Gly Ala
88                       305                   310                   315
89        gaa gcc ttc cgc ccc tta gtc cag act ccg cct gct ccc acc tct gag   1369
90        Glu Ala Phe Arg Pro Leu Val Gln Thr Pro Pro Ala Pro Thr Ser Glu
91                       320                   325                   330
92        atg gtc cca gtc atc agc agt gtg tac ccc ata gca ctt act cgg gcc   1417
93        Met Val Pro Val Ile Ser Ser Val Tyr Pro Ile Ala Leu Thr Arg Ala
94                       335                   340                   345
```

```
 95          gat atg cca atg ggg gcc ccg cag gag atg gaa aag aaa cgg atc ctc        1465
 96          Asp Met Pro Met Gly Ala Pro Gln Glu Met Glu Lys Lys Arg Ile Leu
 97              350             355             360
 98          ctg cca gag aag atc ttg cct tct gaa cga ggt ctg tcc ccc aat aac        1513
 99          Leu Pro Glu Lys Ile Leu Pro Ser Glu Arg Gly Leu Ser Pro Asn Asn
100              365             370             375             380
101          agt gcc cag gac tcc aca gac acc gac agc aac cac gag gat cgc caa        1561
102          Ser Ala Gln Asp Ser Thr Asp Thr Asp Ser Asn His Glu Asp Arg Gln
103                  385             390             395
104          cat ctc tac cag caa agc cac gtg gtc ctc ccc cag gcc cgc aat ggg        1609
105          His Leu Tyr Gln Gln Ser His Val Val Leu Pro Gln Ala Arg Asn Gly
106                  400             405             410
107          atg cct ctt ctg aag gag gtc cct cgc tct ttt gaa ctc ctc aag ccc        1657
108          Met Pro Leu Leu Lys Glu Val Pro Arg Ser Phe Glu Leu Leu Lys Pro
109              415             420             425
110          cct ccc atc tgc ctg agg gac tcc atc aaa gtg atc aac aaa gaa ggg        1705
111          Pro Pro Ile Cys Leu Arg Asp Ser Ile Lys Val Ile Asn Lys Glu Gly
112              430             435             440
113          gag gtg atg gat gtg ttt cga tgt gac cac tgc cac gtc ctc ttc cta        1753
114          Glu Val Met Asp Val Phe Arg Cys Asp His Cys His Val Leu Phe Leu
115          445             450             455             460
116          gat tat gtg atg ttc acc atc cac atg ggg tgc cat ggt ttc cgt gat        1801
117          Asp Tyr Val Met Phe Thr Ile His Met Gly Cys His Gly Phe Arg Asp
118                  465             470             475
119          ccc ttt gag tgt aac atg tgt ggc tat cga agc cac gat cgc tat gag        1849
120          Pro Phe Glu Cys Asn Met Cys Gly Tyr Arg Ser His Asp Arg Tyr Glu
121                  480             485             490
122          ttc tcc tct cac atc gcc aga gga gag cac aga gcc atg ttg aag            1894
123          Phe Ser Ser His Ile Ala Arg Gly Glu His Arg Ala Met Leu Lys
124                  495             500             505
125          tgagcatctg tcctcaatgc gagggtcaac attgtttttt aaagctgatg gtagccttat     1954
126          ccagtagact gaactcaaac ccacctcgag                                      1984
127    <210> SEQ ID NO 2
128    <211> LENGTH: 507
129    <212> TYPE: PRT
130    <213> ORGANISM: Mus musculus
131    <400> SEQUENCE: 2
132          Met Glu Asp Ile Gln Pro Thr Val Glu Leu Lys Ser Thr Glu Glu Gln
133          1               5               10              15
134          Pro Leu Pro Thr Glu Ser Pro Asp Ala Leu Asn Asp Tyr Ser Leu Pro
135                  20              25              30
136          Lys Pro His Glu Ile Glu Asn Val Asp Ser Arg Glu Ala Pro Ala Asn
137                  35              40              45
138          Glu Asp Glu Asp Ala Gly Glu Asp Ser Met Lys Val Lys Asp Glu Tyr
139              50              55              60
140          Ser Asp Arg Asp Glu Asn Ile Met Lys Pro Glu Pro Met Gly Asp Ala
141          65              70              75              80
142          Glu Glu Ser Glu Met Pro Tyr Ser Tyr Ala Arg Glu Tyr Ser Asp Tyr
143                  85              90              95
144          Glu Ser Ile Lys Leu Glu Arg His Val Pro Tyr Asp Asn Ser Arg Pro
```

```
145                   100                 105                 110
146      Thr Ser Gly Lys Met Asn Cys Asp Val Cys Gly Leu Ser Cys Ile Ser
147           115                 120                 125
148      Phe Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Glu Arg Pro
149           130                 135                 140
150      Phe Gln Cys Asn Gln Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn Leu
151      145                 150                 155                 160
152      Leu Arg His Ile Lys Leu His Thr Gly Glu Lys Pro Phe Lys Cys His
153                   165                 170                 175
154      Leu Cys Asn Tyr Ala Cys Gln Arg Arg Asp Ala Leu Thr Gly His Leu
155                   180                 185                 190
156      Arg Thr His Ser Val Glu Lys Pro Tyr Lys Cys Glu Phe Cys Gly Arg
157                   195                 200                 205
158      Ser Tyr Lys Gln Arg Ser Ser Leu Glu Glu His Lys Glu Arg Cys Arg
159           210                 215                 220
160      Ala Phe Leu Gln Asn Pro Asp Leu Gly Asp Ala Ala Ser Val Glu Ala
161      225                 230                 235                 240
162      Arg His Ile Lys Ala Glu Met Gly Ser Glu Arg Ala Leu Val Leu Asp
163                   245                 250                 255
164      Arg Leu Ala Ser Asn Val Ala Lys Arg Lys Ser Ser Met Pro Gln Lys
165                   260                 265                 270
166      Phe Ile Gly Glu Lys Arg His Cys Phe Asp Ala Asn Tyr Asn Pro Gly
167                   275                 280                 285
168      Tyr Met Tyr Glu Lys Glu Asn Glu Met Met Gln Thr Arg Met Met Asp
169           290                 295                 300
170      Gln Ala Ile Asn Asn Ala Ile Ser Tyr Leu Gly Ala Glu Ala Phe Arg
171      305                 310                 315                 320
172      Pro Leu Val Gln Thr Pro Pro Ala Pro Thr Ser Glu Met Val Pro Val
173                   325                 330                 335
174      Ile Ser Ser Val Tyr Pro Ile Ala Leu Thr Arg Ala Asp Met Pro Met
175                   340                 345                 350
176      Gly Ala Pro Gln Glu Met Glu Lys Lys Arg Ile Leu Leu Pro Glu Lys
177           355                 360                 365
178      Ile Leu Pro Ser Glu Arg Gly Leu Ser Pro Asn Asn Ser Ala Gln Asp
179           370                 375                 380
180      Ser Thr Asp Thr Asp Ser Asn His Glu Asp Arg Gln His Leu Tyr Gln
181      385                 390                 395                 400
182      Gln Ser His Val Val Leu Pro Gln Ala Arg Asn Gly Met Pro Leu Leu
183                   405                 410                 415
184      Lys Glu Val Pro Arg Ser Phe Glu Leu Leu Lys Pro Pro Pro Ile Cys
185                   420                 425                 430
186      Leu Arg Asp Ser Ile Lys Val Ile Asn Lys Glu Gly Glu Val Met Asp
187           435                 440                 445
188      Val Phe Arg Cys Asp His Cys His Val Leu Phe Leu Asp Tyr Val Met
189           450                 455                 460
190      Phe Thr Ile His Met Gly Cys His Gly Phe Arg Asp Pro Phe Glu Cys
191      465                 470                 475                 480
192      Asn Met Cys Gly Tyr Arg Ser His Asp Arg Tyr Glu Phe Ser Ser His
193                   485                 490                 495
194      Ile Ala Arg Gly Glu His Arg Ala Met Leu Lys
```

```
195                     500                    505
196    <210> SEQ ID NO 3
197    <211> LENGTH: 26
198    <212> TYPE: DNA
199    <213> ORGANISM: Mus musculus
200    <400> SEQUENCE: 3
201         tactaccatc tcacatgggc tgacca                                    26
202    <210> SEQ ID NO 4
203    <211> LENGTH: 26
204    <212> TYPE: DNA
205    <213> ORGANISM: Mus musculus
206    <400> SEQUENCE: 4
207         gaccagcaca tgttgacact ctgaaa                                    26
208    <210> SEQ ID NO 5
209    <211> LENGTH: 24
210    <212> TYPE: DNA
211    <213> ORGANISM: Mus musculus
212    <400> SEQUENCE: 5
213         gtgtgcgggt tatcctgcat tagc                                      24
214    <210> SEQ ID NO 6
215    <211> LENGTH: 24
216    <212> TYPE: DNA
217    <213> ORGANISM: Mus musculus
218    <400> SEQUENCE: 6
219         atcgaagcag tgccgcttct cacc                                      24
220    <210> SEQ ID NO 7
221    <211> LENGTH: 628
222    <212> TYPE: DNA
223    <213> ORGANISM: Homo sapiens
224    <220> FEATURE:
225    <221> NAME/KEY: CDS
226    <222> LOCATION: (1)...(627)
227    <400> SEQUENCE: 7
228         gaa aga gat gag aat gtt tta aag tca gaa ccc atg gga aat gca gaa    48
229         Glu Arg Asp Glu Asn Val Leu Lys Ser Glu Pro Met Gly Asn Ala Glu
230          1               5                  10                  15
231         gag cct gaa atc cct tac agc tat tca aga gaa tat aat gaa tat gaa    96
232         Glu Pro Glu Ile Pro Tyr Ser Tyr Ser Arg Glu Tyr Asn Glu Tyr Glu
233                        20                  25                  30
234         aac att aag ttg gag aga cat gtt gtc tca ttc gat agt agc agg cca   144
235         Asn Ile Lys Leu Glu Arg His Val Val Ser Phe Asp Ser Ser Arg Pro
236                35                  40                  45
237         acc agt gga aag atg aac tgc gat gtg tgt gga tta tcc tgc atc agc   192
238         Thr Ser Gly Lys Met Asn Cys Asp Val Cys Gly Leu Ser Cys Ile Ser
239             50                  55                  60
240         ttc aat gtc tta atg gtt cat aag cga agc cat act ggt gaa cgc cca   240
241         Phe Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Glu Arg Pro
242             65                  70                  75                  80
243         ttc cag tgt aat cag tgt ggg gca tct ttt act cag aaa ggt aac ctc   288
244         Phe Gln Cys Asn Gln Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn Leu
```

Please Note:
Use I n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields f each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/019,348**

Input Set: **I019348.RAW**

Line	?	Error/Warning	Original Text
733	W	Invalid/Missing Amino Acid Numbering	
982	W	"N" or "Xaa" used: Feature required	Xaa Xaa Ala Ser Asn Val Lys Val Glu Thr G
990	W	"N" or "Xaa" used: Feature required	Lys Leu Lys Cys Asp Ile Cys Gly Ile Xaa C
1002	W	"N" or "Xaa" used: Feature required	Gln Arg Xaa Ser Leu Glu Glu His Lys Glu A
1004	W	"N" or "Xaa" used: Feature required	Glu Ser Met Gly Leu Pro Gly Xaa Xaa ·Xaa P
1006	W	"N" or "Xaa" used: Feature required	Thr Xaa His Xaa Glu Met Ala Glu Asp Leu C
1010	W	"N" or "Xaa" used: Feature required	Ser Ser Met Pro Gln Lys Phe Leu Gly Asp L
1012	W	"N" or "Xaa" used: Feature required	Pro Tyr Asp Ser Ala Xaa Tyr Glu Lys Glu X
1014	W	"N" or "Xaa" used: Feature required	His Val Met Asp Xaa Ala Ile Asn Asn Ala I
1016	W	"N" or "Xaa" used: Feature required	Glu Ser Leu Arg Pro Leu Val Gln Thr Pro P
1018	W	"N" or "Xaa" used: Feature required	Val Pro Val Ile Ser Pro Met Tyr Gln Leu H
1020	W	"N" or "Xaa" used: Feature required	Gly Xaa Pro Arg Ser Asn His Ser Ala Gln A
1022	W	"N" or "Xaa" used: Feature required	Leu Leu Leu Leu Ser Lys Ala Lys Xaa Val X
1024	W	"N" or "Xaa" used: Feature required	Ser Pro Ser Asn Ser Cys Gln Asp Ser Thr A
1026	W	"N" or "Xaa" used: Feature required	Glu Glu Gln Arg Ser Gly Leu Ile Tyr Leu T
1028	W	"N" or "Xaa" used: Feature required	Xaa Ala Xaa Xaa Xaa Xaa Xaa Leu Lys Glu G
1030	W	"N" or "Xaa" used: Feature required	Xaa Leu Arg Ala Ala Ser Glu Asn Ser Gln A
1032	W	"N" or "Xaa" used: Feature required	Ser Thr Ser Gly Glu Gln Xaa Lys Val Tyr L
1034	W	"N" or "Xaa" used: Feature required	Val Leu Phe Leu Asp His Val Met Tyr Thr I
1040	W	"N" or "Xaa" used: Feature required	His Arg Xaa His Xaa Ser